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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Takeda Chemical Industries, Ltd.
(B) STREET: 1-1, Doshomachi 4-chome, Chuo-ku
(C) CITY: Osaka-shi
(D) STATE: Osaka
(E) COUNTRY: Japan
(F) POSTAL CODE (ZIP): 541

(ii) TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof

(iii) NUMBER OF SEQUENCES: 61

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGTGGSCMTS STGGGCAACN YCCTG 25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTNGWRRGGC ANCCAGCAGA KGGCAA 27

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(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCGCSECYM TNRGYATGGA YCGNTAT 27

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CATGTRGWAG GGAANCCAGS AMANRARRAA 30

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTGACYGYTC TNRSNRYTGA CMGVTAC 27

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTGACYGYTC TNRSNRYTGA CMGVTAT 27

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCGCSGCMY TNRGYATGGA YCGNTAC 27

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GATGTGRTAR GGSRNCCAAC AGANGRYAAA 30

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

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(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATGTGRTAR GGSRNCCAAC AGANGRYGAA 30

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GYCACCAACN WSTTCATCCT SWNHCTG 27

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AENSANRAAG SARTAGANGA NRGGRIT 27

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGNTSSTKMT NGSNGTKGTN GGNA 25

- 2 4 2 -

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AYCKGTAYCK GTCCANKGWN ATKGC 25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATKKCCSTG GASAGNTAYN TRGC 24

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GWVGGSAC K CAGCASANGG CRAA 24

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18

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(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: 15th N is A, G, C, or T
6th, 9th, 10th & 12th Ns are inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ARYYTNGCNN TNGCNGAY 18

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS: /
(A) LENGTH: 21
(B) TYPE: Nucleic acid,
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: 13th, 15th, 16th & 18th Ns are
each A, G, C, or T
1st, 4th, 6th Ns are inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

NGGNANCCAR CANANNRNRA A 21

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCTSNTRN SATGWSTGTG GANMGNI 27

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

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(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GAWSNTGMYN ANRTGGWAGG GNANCCA 27

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TAGTGTGTGG AGTCGTGTGG CTGGCTG 27

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AGTCTTTGCT GCCACAGGCA TCCAGCG 27

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CAAGCCAGTA AGGCTATGAA GGGCAGCAAG 30

- 2 4 5 -

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
 Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACAGGACCTG CTGGGCCATC CTGGCGACAC A 31

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn
 1 5 10 15

Phe Ile Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
 20 25 30

Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
 35 40 45

Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
 50 55 60

Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
 65 70 75 80

Val Val Leu Val His Pro Leu Arg Arg Arg Ile
 85 90

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu

- 2 4 6 -

1 5 10 15
 Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly
 20 25 30
 Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg
 35 40 45
 Thr Phe Cys Leu Leu Val Val Val Val Val Val
 50 55

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Ser Ser Thr Thr Arg Gly Pro Arg Val Ser Asp Leu Phe Ser
 1 5 10 15
 Gly Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala
 20 25 30
 Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr
 35 40 45
 Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val
 50 55 60
 Leu Leu Tyr Ser Val Val Val Val Val Gly Leu Val Gly Asn Cys Leu
 65 70 75 80
 Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn
 85 90 95
 Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
 100 105 110
 Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
 115 120 125
 Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
 130 135 140
 Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
 145 150 155 160
 Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser
 165 170 175
 Ala Tyr Ala Val Leu Ala Ile Trp Ala Leu Ser Ala Val Leu Ala Leu

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		180						185					190		
Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val
		195					200					205			
Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu
	210					215					220				
Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Val	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Val
225				230						235					240
Ile	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val
			245						250					255	
Val	Pro	Gly	Cys	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg
			260					265					270		
Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Ala
		275				280							285		
Val	Cys	Trp	Leu	Pro	Leu	His	Val	Phe	Asn	Leu	Leu	Arg	Asp	Leu	Asp
	290					295						300			
Pro	His	Ala	Ile	Asp	Pro	Tyr	Ala	Phe	Gly	Leu	Val	Gln	Leu	Leu	Cys
305					310					315					320
His	Trp	Leu	Ala	Met	Ser	Ser	Ala	Cys	Tyr	Asn	Pro	Phe	Ile	Tyr	Ala
			325						330					335	
Trp	Leu	His	Asp	Ser	Phe	Arg	Glu	Glu	Leu	Arg	Lys	Leu	Leu	Val	Ala
			340					345					350		
Trp	Pro	Arg	Lys	Ile	Ala	Pro	His	Gly	Gln	Asn	Met	Thr	Val	Ser	Val
		355				360						365			
Val	Ile														
	370														

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg	Leu	Tyr	Asn	Val	Thr	Asn
1				5				10						15	
Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	Met	Cys	Thr	Ala
			20					25					30		
Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val

- 2 4 8 -

35	40	45
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr		
50	55	60
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr		
65	70	75
Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser		
	85	90
Ala Tyr Ala Val Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu		
	100	105
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val		
	115	120
Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu		
	130	135
Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val		
145	150	155
Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val		
	165	170
Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg		
	180	185
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val		
	195	200
		205

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser		
1	5	10
Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu		
	20	25
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val		
	35	40
Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile		
	50	55
Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala		
		60

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65		70		75		80									
Ile	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val
				85					90					95	
Val	Pro	Gly	Ser	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg
			100					105					110		
Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Val	Val
			115				120						125		

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CTGGTGCTGG	TGATCGCGCG	GGTGCGCCCG	CTGCACAACG	TGATGAACCT	CCTCATCGGC	60
AACCTGGCCT	TGTCCGACGT	GCTCATGTGC	ACCGCCTGCG	TGCGCTCAC	GCTGGCCTAT	120
GCCTTCGAGC	CACGCGGCTG	GGTGTTCGGC	GGCGGCCTGT	GCCACCTGGT	CTTCTTCCTG	180
CAGCCGGTCA	CCGTCTATGT	GTCGGTGTTT	ACGCTCACCA	CCATCGCAGT	GCACCGGTAC	240
GTCGTGCTGG	TGCACCCGCT	GAGGCGGCCG	ATC			273

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GGCCTGCTGC	TGGTCACCTA	CCTGCTCCCT	CTGCTGGTCA	TCCCTCTGTC	TTACGTCCGG	60
GTGTCAGTGA	AGCTCCGCAA	CCGCGTGGTG	CCGGGCTGCG	TGACCCAGAG	CCAGGCCGAC	120
TGGGACCGCG	CTCGGCGCCG	GCGCACCTTC	TGCTTGCTGG	TGGGGTTCGT	GGTGGTG	177

- 2 5 0 -

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1110
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

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ATGCCCTCAT CGACCACTCG GGGCCCCAGG GTTCTGACT TATTTTCTGG GCTGCCGCCG 60
GCGGTCACAA CTCCCGCCAA CCAGAGCGCA GAGGCCTCGG CGCTCAACGG GTCCGTGGCT 120
GGCGCGGACG CTCCAGCCGT CACGCCCTTC CAGAGCCTGC AGCTGGTGCA TCAGCTGAAG 180
GGGCTGATCG TGCTGCTCTA CAGCGTCGTG GTGGTCGTGG GGCTGGTGGG CAACTGCCCTG 240
CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAACCT CCTCATCGGC 300
AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 360
GCCTTCGAGC CACGCGGCTG GGTGTTTCGGC GCGGGCCTGT GCCACCTGGT CTCTTTCCTG 420
CAGCCGGTCA CCGTCTATGT GTCGGTGTTT ACGCTCACCA CCATCGCAGT GACCGCTAC 480
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCTTCAGCGC CTACGCTGTG 540
CTGGCCATCT GGGCGCTGTC CGCGGTGCTG GCGCTGCCCC CGGCGGTGCA CACCTATCAC 600
GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC 660
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACGTGCTCCC TCTGCTGGTC 720
ATCCTCCTGT CTTACGTCCG GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCTGC 780
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GCGGCACCTT CTGCTTGCTG 840
GTGGTGGTCG TGGTGGTGTT CGCCGTCTGC TGGCTGCCGC TCACAGTCTT CAACCTGCTG 900
CGGACCTCG ACCCCCACGC CATCGACCCT TACGCCTTTG GCTGGTGCA GCTGCTCTGC 960
CACTGGCTCG CCATGAGTTC GGCCTGCTAC AACCCCTTCA TTACGCCTG GCTGCACGAC 1020
AGCTTCCGCG AGGAGCTGCG CAAACTGTTG GTCGCTTGGC CCGCAAGAT ACCCCCCCAT 1080
GGCCAGAATA TGACCGTCAG CGTGGTCATC 1110

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(2) INFORMATION FOR SEQ ID NO: 32:

- 2 5 1 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 618
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGTACAACG TGAAGAATTT CCTCATCGGC 60
AACCTGGCCT TGTCCGACGT GTCATGTGC ACCGCCTGCG TGCTGCTCAC GCTGGCCTAT 120
GCCTTCGAGC CACGCGGCTG GGTGTTCCGC GCGGGCCTGT GCCACCTGGT CTTCTTCCTG 180
CAGGCGGTCA CCGTCTATGT GTCGGTGTTT ACGCTCACCA CCATCGCAGT GGACCGCTAC 240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCTTCAGCGC CTACGCTGTG 300
CTGGCCATCT GGGTGCTGTC CGCGGTGCTG GCGCTGCCCG CCGCCGTGCA CACCTATCAC 360
GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC 420
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCGCTCCC TCTGCTGGTC 480
ATCCTCCTGT CTTACGCCCC GGTGTCAGTG AAGCTCCGCA ACCGCTGGT GCCGCGCCGC 540
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTCCTG 600
GTGGTGCTCG TGGTGGTG 618

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GTGGTTCTGG TGCACCCGCT ACGTCGGCGC ATTTCAGTGA GGCTCAGCGC CTACGCGGTG 60
CTGGGCATCT GGGCTCTATC TGCAGTGCTG GCGCTGCCCG CCGCGGTGCA CACCTACCAT 120
GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TGCGAGGAGT TCTGGGGCTC GCAGGAGCGC 180

- 2 5 2 -

CAACGCCAGA TCTACGCCTG GGGGCTGCTT CTGGGCACCT ATTGCTCCC CCTGCTGGCC 240
 ATCCTCCTGT CTTACGTACG GGTGTCAGTG AAGCTGAGGA ACCGCTGGT GCCTGGCAGC 300
 GTGACCCAGA GTCAAGCTGA CTGGGACCGA GCGCGTCGCC GCCCACTTT CTGTCTGCTG 360
 GTGGTGGTGG TGGTAGTG 378

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Val Cys His Val Ile Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser
 1 5 10 15
 Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met Ile Thr Leu Ile
 20 25 30
 Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe
 35 40 45
 Gly Lys Gly Met Cys His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu
 50 55 60
 His Val Ser Ala Leu Thr
 65 70

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile
 1 5 10 15
 Leu Leu Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg
 20 25 30
 Val Thr Lys Lys Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr
 35 40 45
 Glu Gln Tyr Phe Ala Leu Arg Pro Lys Lys Lys Lys Thr Ile Lys Met
 50 55 60

- 2 5 3 -

Leu Met Leu Val Val Val Leu
65 70

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GTCGTGCATG TCATCTTCAA GAACCAGCGA ATGCACTCGG CCACCAGCCT CTTCATCGTC 60
AACCTGGCAG TTGCCGACAT AATGATCAGC CTGCTCAACA CCCCTTCAC TTTGGTTCGC 120
TTTGTGAACA GCACATGGAT ATTTGGGAAG GGCATGTGCC ATGTCAGCCG CTTTCCCCAG 180
TACTGCTCAC TGCACGTCTC AGCACTGACA 210

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GAGCCAGCTG ACCTCTTCTG GAAGAACCTG GACTTGCCCA CCTTCATCCT GCTCAACATC 60
CTGCCCCCTCC TCATCATCTC TGTGGCCTAC GTTCGTGTGA CCAAGAAACT GTGGCTGTGT 120
AATATGATTG TCGATGTGAC CACAGAGCAG TACTTTGCCC TGGGGCCCAA AAAGAAGAAG 180
ACCATCAAGA TGTTGATGCT GGTGGTAGTC CTC 213

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

- 2 5 4 -

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala Trp Val Val Cys
 1 5 10 15
 Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu Pro Thr Ala Val
 20 25 30
 Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val Cys Tyr Asp Leu
 35 40 45
 Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr Gly Met Ala Leu
 50 55 60
 Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu Leu Ala Cys Tyr
 65 70 75 80
 Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly Pro Ala Gly Pro
 85 90 95
 Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met Ala Val Val Val
 100 105 110
 Ala Ala Val
 115

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Met Glu Gln Asp Asn Gly Thr Ile Gln Ala Pro Gly Leu Pro Pro Thr
 1 5 10 15
 Thr Cys Val Tyr Arg Glu Asp Phe Lys Arg Leu Leu Leu Thr Pro Val
 20 25 30
 Tyr Ser Val Val Leu Val Val Gly Leu Pro Leu Asn Ile Cys Val Ile
 35 40 45
 Ala Gln Ile Cys Ala Ser Arg Arg Thr Leu Thr Arg Ser Ala Val Tyr
 50 55 60
 Thr Leu Asn Leu Ala Leu Ala Asp Leu Met Tyr Ala Cys Ser Leu Pro
 65 70 75 80

- 2 5 5 -

Leu Leu Ile Tyr Asn Tyr Ala Arg Gly Asp His Trp Pro Phe Gly Asp
85 90 95

Leu Ala Cys Arg Phe Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly
100 105 110

Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile
115 120 125

Cys His Pro Leu Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala
130 135 140

Trp Val Val Cys Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu
145 150 155 160

Pro Thr Ala Val Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val
165 170 175

Cys Tyr Asp Leu Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr
180 185 190

Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu
195 200 205

Leu Ala Cys Tyr Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly
210 215 220

Pro Ala Gly Pro Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met
225 230 235 240

Ala Val Val Val Ala Ala Val Phe Ala Ile Ser Phe Leu Pro Phe His
245 250 255

Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val Ser
260 265 270

Cys Pro Val Leu Glu Thr Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro
275 280 285

Phe Ala Ser Val Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr
290 295 300

Gln Gln Lys Phe Arg Arg Gln Pro His Asp Leu Leu Gln Arg Leu Thr
305 310 315 320

Ala Lys Trp Gln Arg Gln Arg Val
325

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

- 2 5 6 -

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

GCTTCCTGGC ACAAGCGTGG AGGTCGCCGT GCTGCTTGGG TAGTGTGTGG AGTCGTGTGG   60
CTGGCTGTGA CAGCCCAGTG CCTGCCCACG GCAGTCTTTG CTGCCACAGG CATCCAGCGC   120
AACCGCACTG TGTGCTACGA CCTGAGCCCA CCCATCCTGT CTACTCGCTA CCTGCCCTAT   180
GGTATGGCCC TCACGGTCAT CGGCTTCTTG CTGCCCTTCA TAGCCTTACT GGCTTGTTAT   240
TGTCGCATGG CCCGCCGCCT GTGTCGCCAG GATGGCCCAG CAGATCCTGT GGCCCAAGAG   300
CGGCGCAGCA AGGCGGCTCG TATGGCTGTG GTGGTGGCAG CTGTC   345

```

(2) INFORMATION FOR SEQ ID NO: 41:

(1) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH:      984
(B) TYPE:        Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY:    Linear

```

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

ATGGAGCAGG ACAATGGCAC CATCCAGGCT CCAGGCTTGC CGCCACACCAC CTGCGTCTAC   60
CGTGAGGATT TCAAGCGACT GCTGCTAACC CCGGTATACT CGGTGGTGCT GGTGGTCGGC   120
CTGCCACTGA ACATCTGCGT CATTGCCCAG ATCTGCGCAT CCAGCCGGAC CGTGACCCGT   180
TCCGCTGTGT ACACCCTGAA CCTGGCACTG GCGGACCTGA TGTATGCCTG TTCACTACCC   240
CTACTTATCT ATAACTACGC CAGAGGGGAC CACTGGCCCT TCGAGACCT CGCCTGCCGC   300
TTTGTACGCT TCCTCTTCTA TGCCAATCTA CATGGCAGCA TCCTGTTCCT CACCTGCATT   360
AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCCCTGGCTT CCTGGCACAA GCGTGGAGGT   420
CGCCGTGCTG CTTGGGTAGT GTGTGGAGTC GTGTGGCTGG CTGTGACAGC CCAGTGCCTG   480
CCCACGGCAG TCTTTGCTGC CACAGGCATC CAGCGCAACC GCACTGTGTG CTACGACCTG   540
AGCCCACCCA TCCTGTCTAC TCGCTACCTG CCCTATGGTA TGGCCCTCAC GGTTCATCGGC   600
TTCTTGCTGC CCTTCATAGC CTTACTGGCT TGTATTGTG GCAATGGCCCG CCGCCTGTGT   660

```

- 2 5 7 -

CGCCAGGATG GCCCAGCAGG TCCTGTGGCC CAAGAGCGGC GCAACCAAGGC GGCTCGTATG 720
 GCTGTGGTGG TGGCAGCTGT CTTTGCCATC AGCTTCCTGC CTTTCCACAT CACCAAGACA 780
 GCCTACTTGG CTGTGCGCTC CACGCCCCGGT GTCTCTTGCC CTGTGCTGGA GACCTTCGCT 840
 GCTGCCTACA AAGGCACTCG GCCCTTCGCC AGTGTCAACA GTGTCTGGA CCCCATTCCTC 900
 TTCTACTTCA CACAACAGAA GTCCGGCGG CAACCCACG ATCTCTTACA GAGGCTCACA 960
 GCCAAGTGGC AGAGGCAGAG AGTC 984

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Ala Ala Met Ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg
 1 5 10 15
 Ser Ser Ser Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe
 20 25 30
 Ile Trp Ala Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr His Gln
 35 40 45
 Arg Leu Phe His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu Gln Trp
 50 55 60
 Pro Asn Lys Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe
 65 70 75 80
 Gly Tyr Leu Leu Pro Leu Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val
 85 90 95
 Leu Asn His Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu
 100 105 110
 Ala Ser Lys Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val Val
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

- 2 5 8 -

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

GCCGCGATGT CTGTGGATCG CTACGTGGCC ATTGTGCACT CGCGGCGCTC CTCTCCCTC      60
AGGGTGTCCC GCAACGCACT GCTGGGCGTG GGCTTCATCT GGCGCGTGTG CATCGCCATG      120
GCCTCGCCGG TGGCCTACCA CCAGCGTCTT TTCCATCGGG ACACCAACCA CACCTTCTGC      180
TGGGAGCAGT GGCCCAACAA GCTCCACAAG AAGGCTTACG TGGTGTGCAC TTTCGTCTTT      240
GGGTACCTTC TGCCCTTACT GCTCATCTGC TTTTGCTATG CCAAGGTCCT TAATCATCTG      300
CATAAAAAGC TGAAAAACAT GTCAAAAAG TCTGAACCAT CCAAGAAAAA GACTGCACAG      360
ACCGTCCTGG TGGTCGTTGT AGTA                                          384

```

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH:      71
(B) TYPE:        Amino acid
(C) TOPOLOGY:    Linear

```

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

Val Leu Trp Phe Phe Gly Phe Ser Ile Lys Arg Thr Pro Phe Ser Val
 1              5              10              15
Tyr Phe Leu His Leu Ala Ser Ala Asp Gly Ala Tyr Leu Phe Ser Lys
      20              25              30
Ala Val Phe Ser Leu Leu Asn Ala Gly Gly Phe Leu Gly Thr Phe Ala
      35              40              45
His Tyr Val Arg Ser Val Ala Arg Val Leu Gly Leu Cys Ala Phe Val
      50              55              60
Ala Gly Val Ser Leu Leu Pro
65              70

```

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH:      215
(B) TYPE:        Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY:    Linear

```

(ii) MOLECULE TYPE: cDNA

- 2 5 9 -

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

GTGCTCTGGT TCTTCGGCTT CTCCATCAAG AGGACCCCCT TCTTCGTCTA CTTCCTGCAC      60
CTGGCCAGCG CCGACGGCGC CTACCTCTTC AGCAAGGCCG TGTTCCTCCCT GCTGAACGCC      120
GGCGGCTTCC TGGGCACCTT CGCCCACTAT GTGCGCAGCG TGGCCCCGGT GCTGGGGCTC      180
TGGGCTTTCG TGGCGGGCGT GAGCCTCCTG CCGGC                                215

```

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH:      348
(B) TYPE:        Amino acid
(C) TOPOLOGY:    Linear

```

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

Met Glu Leu Ala Met Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro
 1              5              10              15
Glu Pro Pro Ala Pro Glu Ser Arg Pro Leu Phe Gly Ile Gly Val Glu
      20              25              30
Asn Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val
      35              40              45
Leu Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly
      50              55              60
Lys Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala
      65              70              75              80
Asp Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr
      85              90              95
Ala Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His
      100             105             110
Tyr Phe Phe Thr Val Ser Met Leu Val Ser Ile Phe Thr Leu Ala Ala
      115             120             125
Met ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg Ser Ser
      130             135             140
Ser Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe Ile Trp
      145             150             155             160
Ala Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr His Gln Arg Leu
      165             170             175

```

- 2 6 0 -

Phe His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu Gln Trp Pro Asn
 180 185 190
 Lys Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe Gly Tyr
 195 200 205
 Leu Leu Pro Leu Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val Leu Asn
 210 215 220
 His Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu Ala Ser
 225 230 235 240
 Lys Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val Val Phe Gly
 245 250 255
 Ile Ser Trp Leu Pro His His Val Val His Leu Trp Ala Glu Phe Gly
 260 265 270
 Ala Phe Pro Leu Thr Pro Ala Ser Phe Phe Phe Arg Ile Thr Ala His
 275 280 285
 Cys Leu Ala Tyr Ser Asn Ser Ser Val Asn Pro Ile Ile Tyr Ala Phe
 290 295 300
 Leu Ser Glu Asn Phe Arg Lys Ala Tyr Lys Gln Val Phe Lys Cys His
 305 310 315 320
 Val Cys Asp Glu Ser Pro Arg Ser Glu Thr Lys Glu Asn Lys Ser Arg
 325 330 335
 Met Asp Thr Pro Pro Ser Thr Asn Cys Thr His Val
 340 345

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1044
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATGGAAGTGG CTATGGTGAA CCTCAGTGAA GGAATGGGA GCGACCCAGA GCCGCCAGCC 60
 CCGGAGTCCA GGCCGCTCTT CGGCATTGGC GTGGAGAACT TCATTACGCT GGTAGTGTTC 120
 GGCTTGATTT TCGCGATGGG CGTGCTGGGC AACAGCCTGG TCATCACCGT GCTGGCGCGC 180
 AGCAAACCAG GCAACCCCGG CAGCACCACC AACCTGTGTTA TCATCAATCT GAGCATCGCA 240

- 2 6 1 -

GACCTGGCCT ACCTGCTCTT CTGCATCCCT TTTCAGGCCA CCGTGTATGC ACTGCCACCC 300
 TGGGTGCTGG GCGCCTTCAT CTGCAAGTTT ATACACTACT TCTTCACCGT GTCCATGCTG 360
 GTGAGCATCT TCACCCTGGC CCGGATGTCT GTGGATCGCT ACCTGGCCAT TGTGCACTCG 420
 CGGCGCTCCT CCTCCCTCAG GGTGTCCCGC AACGCACTGC TGGGCGTGGG CTTCATCTGG 480
 GCGCTGTCCA TCGCCATGGC CTCGCCGGTG GCCTACCACC AGCTCTTTT CCATCCGGAC 540
 AGCAACCAGA CCTTCTGCTG GGAGCAGTGG CCCAACAAGC TCCACAAGAA GGCTTACGTG 600
 GTGTGCACTT TCGTCTTTGG GTACCTTCTG CCCTTACTGC TCATCTGCTT TTGCTATGCC 660
 AAGGTCCTTA ATCATCTGCA TAAAAAGCTG AAAAACATGT CAAAAAAGTC TGAAGCATCC 720
 AAGAAAAAGA CTGCACAGAC CGTCCTGGTG GTCGTTGTAG TATTTGGCAT ATCCTGGCTG 780
 CCCCATCATG TCGTCCACCT CTGGGCTGAG TTTGGAGCCT TCCCACTGAC GCCAGCTTCC 840
 TTCTTCTTCA GAATCACCGC CCATTGCCTG GCATACAGCA ACTCCTCAGT GAACCCCATC 900
 ATATATGCCT TTCTCTCAGA AAAGTTCCGG AAGGCGTACA AGCAAGTGTT CAAGTGTCAT 960
 GTTTGCGATG AATCTCCACG CAGTGAACT AAGGAAAACA AGAGCCGGAT GGACACCCCG 1020
 CCATCCACCA ACTGCACCCA CGTG 1044

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Leu Leu Thr Leu His Pro Val Trp Ser Gln Lys His Arg Thr Ser His
 1 5 10 15
 Trp Ala Ser Arg Val Val Leu Gly Val Trp Leu Ser Ala Thr Ala Phe
 20 25 30
 Ser Val Pro Tyr Leu Val Phe Arg Glu Thr Tyr Asp Asp Arg Lys Gly
 35 40 45
 Arg Val Thr Cys Arg Asn Asn Tyr Ala Val Ser Thr Asp Trp Glu Ser
 50 55 60
 Lys Glu Met Gln Thr Val Arg Gln Trp Ile His Ala Thr Cys Phe Ile
 65 70 75 80
 Ser Arg Phe Ile Leu Gly Phe Leu Leu Pro Phe Leu Val Ile Gly Phe

- 2 6 2 -

	85	90	95
Cys Tyr Glu Arg Val Ala Arg Lys Met Lys Glu Arg Gly Leu Phe Lys			
	100	105	110
Ser Ser Lys Pro Phe Lys Val Thr Met Thr Ala Val Ile			
	115	120	125

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

CTTCTCACCC TTCACCCAGT GTGGTCCCAA AAGCACCGAA CCTCACACTG GGCTTCCAGA    60
GTCGTTCCTGG GAGTCTGGCT CTCTGCCACT GCCTTCAGCG TGCCTATTTT GGTTTTCAGG    120
GAGACATATG ATGACCGTAA AGGAAGAGTG ACCTGCAGAA ATAACTACGC TGTGTCCACT    180
GACTGGGAAA GCAAAGAGAT GCAAACAGTA AGACAATGGA TTGATGCCAC CTGTTTCATC    240
AGCCGCTTCA TACTGGGCTT CCTTCTGCCT TTCTTAGTCA TTGCTTTTGG TTATGAAAGA    300
GTAGCCCGCA AGATGAAAGA GAGGGGCCCTC TTAAATCCA GCAAAACCCTT CAAAGTCACG    360
ATGACTGCTG TTATCTC                                     377
  
```

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Phe Lys Ile Val Lys Pro Leu Ser Thr Ser Phe Ile Gln Ser Val Asn	
1 5 10 15	
Tyr Ser Lys Leu Val Ser Leu Val Val Trp Leu Leu Met Leu Leu Leu	
20 25 30	
Ala Val Pro Asn Val Ile Leu Thr Asn Gln Arg Val Lys Asp Val Thr	
35 40 45	

- 2 6 3 -

Gln Ile Lys Cys Met Glu Leu Lys Asn Glu Leu Gly Arg Gln Trp His
 50 55 60
 Lys Ala Ser Asn Tyr Ile Phe Val Gly Ile Phe Trp Leu Val Phe Leu
 65 70 75 80
 Leu Leu Ile Ile Phe Tyr Thr Ala Ile Thr Arg Lys Ile Phe Lys Ser
 85 90 95
 His Leu Lys Ser Arg Lys Asn Ser Ile Ser Val Lys Lys Lys Ser Ser
 100 105 110
 Arg Asn Ile Phe Ser Ile Val
 115

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TTCAAGATTG TGAAGCCCCT TTCCACGTCC TTCATCCAGT CTGTGAACTA CAGCAAACCTC 60
 GTCTCGCTGG TGGTCTGGTT GCTCATGCTC CTCCTCGCCG TCCTCAACGT CATTCTCACC 120
 AACCAGAGAG TTAAGGACGT GACGCAGATA AAATGCATGG AACCTAAAAA CCAACTGGGC 180
 CGCCAGTGGC ACAAGGCGTC AACTACATC TTTGTGGGCA TTTCTCTGGCT TGTGTTCCTT 240
 TTGCTAATCA TTTTCTACAC TGCTATCACC AGGAAAATCT TTAAGTCCCA CCTGAAATCC 300
 AGAAAGAATT CCATCTCGGT CAAAAGAAA TCTAGCCGCA ACATCTTCAG CATCGTG 357

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu Ala Met Leu Ser
 1 5 10 15

- 2 6 4 -

Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu Val Ala Cys Arg
 20 25 30
 Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu Ala Ile Leu Ser
 35 40 45
 Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val Val His Pro Met
 50 55 60
 Arg Tyr Glu Val Arg Met Lys Leu Gly Leu Val Ala Ser Val Leu Val
 65 70 75 80
 Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val Pro Val Leu Gly
 85 90 95
 Arg Val Ser Trp Glu Glu Gly Pro Pro Ser Val Pro Pro Gly Cys Ser
 100 105 110
 Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe Val Val Val Phe
 115 120 125
 Ala Val Leu Tyr Phe Leu Leu Pro Leu Leu Leu Ile Leu Val Val Tyr
 130 135 140
 Cys Ser Met Phe Arg Val Ala Arg Val Ala Ala Met Gln His Gly Pro
 145 150 155 160
 Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser Glu Ser Leu Ser
 165 170 175
 Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro Gln Thr Thr Pro
 180 185 190
 His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val Val Leu Leu Ala Val
 195 200 205
 Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe Ser Phe His Leu
 210 215 220
 Tyr Val Ala Leu Ser Ala Gln Pro Ile Ala Ala Gly Gln Val Glu Asn
 225 230 235 240
 Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser
 245 250

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

- 2 6 5 -

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

GTGGACCTGC TGGCTGCCCT GACCCTCATG CCTCTGGCCA TGCTCTCCAG CTCGGCCCTC 60
TTTGACCACG CCCTCTTTGG GGAGGTGGCC TGCCGCCTCT ACTTGTTCCT GAGCGTCTGC 120
TTTGTCAGCC TGGCCATCCT CTCGGTGTCC GCCATCAATG TGGAGCGCTA CTATTATGTG 180
GTCCACCCCA TGGCCTATGA GGTGCGCATG AAAGTGGGGC TGGAGGCCTC TGTGCTGGTG 240
GGCGTGTGGG TGAAGGCCCT GGCCATGGCT TCTGTGCCAG TGTAGGGAAG GGTGTCTCTG 300
GAGGAAGGCC CTCCCAGTGT CCCCCAGGC TGTTCACTCC AATGGAGCCA CAGTGCCTAC 360
TGCCAGCTTT TCGTGGTGGT CTTCGCCGTC CTCTACTTCC TGGTGGCCCT GCTCCTCATC 420
CTTGTGGTCT ACTGCAGCAT GTTCCGGGTG GCTCGTGTGG CTGCCATGCA GCACGGGCCG 480
CTGCCCACGT GGATGGAGAC GCCCCGGCAA CGCTCCGAGT CTCACAGCAG CCGCTCCACT 540
ATGGTCACCA GCTCGGGGGC CCCGCAGACC ACCCCTCACC GGAAGTTTGG CCGAGGGAAG 600
GCAGCAGTGG TCCTCCTGGC TGTGGGAGGA CAGTTCCTGC TCTTTTGGTT GCCCTACTTC 660
TCCCTCCACC TCTATGTGGC CCTGAGCGCT CAGCCCATTG CAGCGGGGCA GGTGGAGAAC 720
GTGGTGGACCT GGATTGGCTA CTTCTGCTTC ACCTCC 756

```

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

Ala Asp Val Leu Val Thr Ala Ile Cys Leu Pro Ala Ser Leu Leu Val
1           5           10           15
Asp Ile Thr Glu Ser Trp Leu Phe Gly His Ala Leu Cys Lys Val Ile
20           25           30
Pro Tyr Leu Gln Ala Val Ser Val Ser Val Val Val Leu Thr Leu Ser
35           40           45
Ser Ile Ala Leu Asp Arg Trp Tyr Ala Ile Cys His Pro Leu Leu Phe
50           55           60
Lys Ser Thr Ala Arg Arg Ala Arg Gly Ser Ile Leu Gly Ile Trp Ala
65           70           75           80

```

- 2 6 6 -

Val Ser Leu Ala Val Met Val Pro Gln Ala Ala Val Met Glu Cys Ser
85 90 95

Ser Val Leu Pro Glu Leu Ala Asn Arg Thr Arg Leu Leu Ser Val Cys
100 105 110

Asp Glu Arg Trp Ala Asp Asp Leu Tyr Pro Lys Ile Tyr His Ser Cys
115 120 125

Phe Phe Ile Val Thr Tyr Leu Ala Pro Leu Gly Leu Met Ala Met Ala
130 135 140

Tyr Phe Gln Ile Phe Arg Lys Leu Trp Gly Arg Gln Ile Pro Gly Thr
145 150 155 160

Thr Ser Ala Leu Val Arg Asn Trp Lys Arg Pro Ser Asp Gln Leu Asp
165 170 175

Asp Gln Gly Gln Gly Leu Ser Ser Glu Pro Gln Pro Arg Ala Arg Ala
180 185 190

Phe Leu Ala Glu Val Lys Gln Met Arg Ala Arg Arg Lys Thr Ala Lys
195 200 205

Met Leu Met Val Val Leu Leu Val Phe Ala Leu Cys Tyr Leu Pro Ile
210 215 220

Ser Val Leu Asn Val Leu Lys Arg Val Phe Gly Met Phe Arg Gln Ala
225 230 235 240

Ser Asp Arg Glu Ala Ile Tyr Ala Cys Phe Thr Phe Ser His Trp Leu
245 250 255

Val Tyr Ala Asn Ser Ala Ala
260

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55.

GCCGATGTGC TGGTGACAGC CATCTGCCTG CCGGCCAGTC TGCTGGTAGA CATCACGGAA 60

TCCTGGCTCT TTGGCCATGC CCTCTGCAAG GTCATCCCCT ATCTACAGGC CGTGTCGGTG 120

- 2 6 7 -

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TCAGTGGTCG TGCTGACTCT CAGCTCCATC GCCCTGGACC GCTGGTACGC CATCTGCCAC 180
CCGCTGTTGT TCAAGAGCAC TGCCCGGCGC GCCCGCGGCT CCGTCCTCGG CATCTEGGCG 240
GTGTCGCTGG CTGTCATGGT GCCTCAGGCT GCTGTCATGG AGTGTAGCAG CGTGCCTGCC 300
GAGCTGGCCA ACCGCACCCG CCTCCTGTCT GTCTGTGATG AGTGTGGGC AGACGACCTG 360
TACCCCAAGA TCTACCACAG CTGCTTCTTC ATTGTCACCT ACCTGGCCCC ACTGGGCCTC 420
ATGGCCATGG CCTATTTCCA GATCTTCCGC AAGCTCTGGG GCGGCCAGAT CCGCGGCACC 480
ACCTCGGCCC TGGTGCGCAA CTGGAAGCGG CCCTCAGACC AGCTGGACGA CCAGGGCCAG 540
GGCCTGAGCT CAGAGCCCCA GCCCGGGGCC CGCGCCTTCC TGCCCGAGGT GAAACAGATG 600
CGAGCCCCGA GGAAGACGGC CAAGATGCTG ATGGTGGTGC TGTGGTCTT CGCCCTCTGC 660
TACCTGCCCA TCAGTGTCTT CAACGTCCTC AAGAGGGTCT TCGGGATGTT CCGCCAAGCC 720
AGCGACCGAG AGGCCATCTA CGCCTGCTTC ACCTTCTCCC ACTGGCTGGT GTACGCCAAC 780
AGCGCCGCC 789

```

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

Met Glu Trp Asp Asn Gly Thr Gly Gln Ala Leu Gly Leu Pro Pro Thr
 1             5             10             15
Thr Cys Val Tyr Arg Glu Asn Phe Lys Gln Leu Leu Leu Pro Pro Val
 20             25             30
Tyr Ser Ala Val Leu Ala Ala Gly Leu Pro Leu Asn Ile Cys Val Ile
 35             40             45
Thr Gln Ile Cys Thr Ser Arg Arg Ala Leu Thr Arg Thr Ala Val Tyr
 50             55             60
Thr Leu Asn Leu Ala Leu Ala Asp Leu Leu Tyr Ala Cys Ser Leu Pro
 65             70             75             80
Leu Leu Ile Tyr Asn Tyr Ala Gln Gly Asp His Trp Pro Phe Gly Asp
 85             90             95
Phe Ala Cys Arg Leu Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly
 100            105            110

```

- 2 6 8 -

Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile
 115 120 125
 Cys His Pro Leu Ala Pro Trp His Lys Arg Gly Gly Arg Arg Ala Ala
 130 135 140
 Trp Leu Val Cys Val Thr Val Trp Leu Ala Val Thr Thr Gln Cys Leu
 145 150 155 160
 Pro Thr Ala Ile Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val
 165 170 175
 Cys Tyr Asp Leu Ser Pro Pro Ala Leu Ala Thr His Tyr Met Pro Tyr
 180 185 190
 Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ala Ala Leu
 195 200 205
 Leu Ala Cys Tyr Cys Leu Leu Ala Cys Arg Leu Cys Arg Gln Asp Gly
 210 215 220
 Pro Ala Glu Pro Val Ala Gln Glu Arg Arg Gly Lys Ala Ala Arg Met
 225 230 235 240
 Ala Val Val Val Ala Ala Ala Phe Ala Ile Ser Phe Leu Pro Phe His
 245 250 255
 Ile Thr Lys Thr Ala Tyr Leu Ala Val Gly Ser Thr Pro Gly Val Pro
 260 265 270
 Cys Thr Val Leu Glu Ala Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro
 275 280 285
 Phe Ala Ser Ala Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr
 290 295 300
 Gln Lys Lys Phe Arg Arg Arg Pro His Glu Leu Leu Gln Lys Leu Thr
 305 310 315 320
 Ala Lys Trp Gln Arg Gln Gly Arg
 325

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

- 2 6 9 -

```

ATGGAATGGG ACAATGGCAC AGGCCAGGCT CTGGGCTTGC CACCCACCAC CTGTGTCTAC      60
CGCGAGAACT TCAAGCAACT GCTGCTGCCA CCTGTGTATT CGGCGGTGCT GCGGGCTGGC      120
CTGCCGCTGA ACATCTGTGT CATTACCCAG ATCTGCACGT CCCC,CCGGGC CCTGACCCGC      180
ACGGCCGTGT ACACCCTAAA CCTTGCTCTG GCTGACCTGC TATATGCCTG CTCCTTGCCC      240
CTGCTCATCT ACAACTATGC CCAAGGTGAT CACTGGCCCT TTGACGACTT CGCCTGCCGC      300
CTGGTCCGCT TCCTCTTCTA TGCCAACCTG CACGGCAGCA TCCCTTTCCT CACCTGCATC      360
AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCGCTGGCCC CCTGACACAA ACGTGGGGGC      420
CGCCGGGCTG CCTGGCTAGT GTGTGTAACC GTGTGGCTGG CCGTGACAAC CCAGTGCCTG      480
CCCACAGCCA TCTTCGCTGC CACAGGCATC CAGCGTAACC GCACTGTCTG CTATGACCTC      540
AGCCCGCCTG CCCTGGCCAC CCACTATATG CCCTATGGCA TGGCTCTCAC TGTATCGGC      600
TTCCTGCTGC CCTTTGCTGC CCTGCTGGCC TGCTACTGTC TCCGGGCCTG CCGCCTGTGC      660
CGCCAGGATG GCCCGGCAGA GCCTGTGGCC CAGGAGCGGC GTGCAAGGC GGCCCGCATG      720
GCCGTGGTGG TGGCTGCTGC CTTTGCCATC AGCTTCCTGC CTTTTCACAT CACCAAGACA      780
GCCTACCTGG CAGTGGGCTC GACGCCGGGC GTCCCCTGCA CTGTATTGGA GGCCTTTGCA      840
GCGGCCATCA AAGGCACGCG GCCGTTTGCC AGTGCCAACA GCGTGTGGA CCCCATCCTC      900
TTCTACTTCA CCCAGAAGAA GTTCGCGCGG CGACCACATG AGCTCCTACA GAAACTCACA      960
GCCAATGGC AGAGGCAGGG TCGC                                     984

```

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH:      26
(B) TYPE:         Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY:     Linear

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(ii) MOLECULE TYPE:  Other nucleic acid
                    Synthetic DNA

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

ACAGCCATCT TCGCTGCCAC AGGCAT 26

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH:      29
(B) TYPE:         Nucleic acid
(C) STRANDEDNESS: Single

```


- 2 7 0 -

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

AGACAGTAGC AGGCCAGCAG GGCAGCAA 29

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

CTGTGYGYSA TYGCNNTKGA YMGSTAC 27

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

AKGWAGWAGG GCAGCCAGCA GANSRYGAA 29